

SEQUENCE LISTING

<110> Winslow, Barbara J.
Cochran, Mark D.

<120> Recombinant Virus Expressing Foreign DNA Encoding
Feline CD80, Feline CD86, Feline CD28, Feline CTLA-4 or
Feline Interferon-gama And Uses Thereof

<130> 54957-B

<140> Not Yet Known

<141> 1999-04-30

<150> 60/083,870

<151> 1998-05-01

<160> 82

<170> PatentIn Ver. 2.0

<210> 1

<211> 941

<212> DNA

<213> feline CD80

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<221> CDS

<222> (1)..(876)

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ccc aag ctc ttt ccg ctc ttg atg cta gct agt ctt ttt tac ttc tgt	96
Pro Lys Leu Phe Pro Leu Leu Met Leu Ala Ser Leu Phe Tyr Phe Cys	
20 25 30	

tca ggt atc atc cag ggg aac aag aca gtg gaa gaa gta gca gta cta	144
Ser Gly Ile Ile Gln Val Asn Lys Thr Val Glu Glu Val Ala Val Leu	
35 40 45	

tcc tgt gat tac aac att tcc acc aaa gaa ctg acg gaa att cga atc	192
Ser Cys Asp Tyr Asn Ile Ser Thr Lys Glu Leu Thr Glu Ile Arg Ile	
50 55 60	

tat tgg caa aag gat gat gaa atg gtg ttg gct gtc atg tct ggc aaa	240
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*Cancelled
Per
Amend B*

09303510.043099

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Val	Gln	Val	Trp	Pro	Lys	Tyr	Lys	Asn	Arg	Thr	Phe	Thr	Asp	Val	Thr	
				85					90					95		
gat	aac	cac	tcc	att	gtg	atc	atg	gct	ctg	cgc	ctg	tca	gac	aat	ggc	336
Asp	Asn	His	Ser	Ile	Val	Ile	Met	Ala	Leu	Arg	Leu	Ser	Asp	Asn	Gly	
			100					105					110			
aaa	tac	act	tgt	att	att	caa	aag	att	gaa	aaa	ggg	tct	tac	aaa	gtg	384
Lys	Tyr	Thr	Cys	Ile	Ile	Gln	Lys	Ile	Glu	Lys	Gly	Ser	Tyr	Lys	Val	
			115					120				125				
aaa	cac	ctg	act	tcg	gtg	atg	tta	ttg	gtc	aga	gct	gac	ttc	cct	gtc	432
Lys	His	Leu	Thr	Ser	Val	Met	Leu	Leu	Val	Arg	Ala	Asp	Phe	Pro	Val	
			130				135				140					
cct	agt	ata	act	gat	ctt	gga	aat	cca	tct	cat	aac	atc	aaa	agg	ata	480
Pro	Ser	Ile	Thr	Asp	Leu	Gly	Asn	Pro	Ser	His	Asn	Ile	Lys	Arg	Ile	
					145		150				155				160	
atg	tgc	tta	act	tct	gga	ggt	ttt	cca	aag	cct	cac	ctc	tcc	tgg	ctg	528
Met	Cys	Leu	Thr	Ser	Gly	Gly	Phe	Pro	Lys	Pro	His	Leu	Ser	Trp	Leu	
					165				170					175		
gaa	aat	gaa	gaa	gaa	tta	aat	gcc	atc	aac	aca	aca	gtt	tcc	caa	gat	576
Glu	Asn	Glu	Glu	Glu	Leu	Asn	Ala	Ile	Asn	Thr	Thr	Val	Ser	Gln	Asp	
				180				185					190			
cct	gaa	act	gag	ctc	tac	act	att	agc	agt	gaa	ctg	gat	ttc	aat	atg	624
Pro	Glu	Thr	Glu	Leu	Tyr	Thr	Ile	Ser	Ser	Glu	Leu	Asp	Phe	Asn	Met	
				195				200				205				
aca	aac	aac	cat	agc	ttc	ctg	tgt	ctt	gtc	aag	tat	gga	aac	tta	cta	672
Thr	Asn	Asn	His	Ser	Phe	Leu	Cys	Leu	Val	Lys	Tyr	Gly	Asn	Leu	Leu	
				210			215				220					
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Val	Ser	Gln	Ile	Phe	Asn	Trp	Gln	Lys	Ser	Glu	Pro	Gln	Pro	Ser	Asn	
				225		230				235					240	
aat	cag	ctc	tgg	atc	att	atc	ctg	agc	tca	gta	gta	agt	ggg	att	gtt	768
Asn	Gln	Leu	Trp	Ile	Ile	Ile	Leu	Ser	Ser	Val	Val	Ser	Gly	Ile	Val	
				245				250					255			
gtg	atc	act	gca	ctt	acc	tta	aga	tgc	cta	gtc	cac	aga	cct	gct	gca	816

Val Ile Thr Ala Leu Thr Leu Arg Cys Leu Val His Arg Pro Ala Ala
260 265 270

agg tgg aga caa aga gaa atg ggg aga gcg cgg aaa tgg aaa aga tct 864
Arg Trp Arg Gln Arg Glu Met Gly Arg Ala Arg Lys Trp Lys Arg Ser
275 280 285

cac ctg tct aca tagattctgc agaaccactg tatgcagagc atctggaggt 916
His Leu Ser Thr
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agcctcttta gctcttctct actag 941

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35 40 45

Ser Cys Asp Tyr Asn Ile Ser Thr Lys Glu Leu Thr Glu Ile Arg Ile
50 55 60

Tyr Trp Gln Lys Asp Asp Glu Met Val Leu Ala Val Met Ser Gly Lys
65 70 75 80

Val Gln Val Trp Pro Lys Tyr Lys Asn Arg Thr Phe Thr Asp Val Thr
85 90 95

Asp Asn His Ser Ile Val Ile Met Ala Leu Arg Leu Ser Asp Asn Gly
100 105 110

Lys Tyr Thr Cys Ile Ile Gln Lys Ile Glu Lys Gly Ser Tyr Lys Val
115 120 125

Lys His Leu Thr Ser Val Met Leu Leu Val Arg Ala Asp Phe Pro Val
130 135 140

Pro Ser Ile Thr Asp Leu Gly Asn Pro Ser His Asn Ile Lys Arg Ile

145

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09303510 043099

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	180			185		190
Pro Glu Thr Glu Leu Tyr Thr Ile Ser Ser Glu Leu Asp Phe Asn Met						
	195			200		205
Thr Asn Asn His Ser Phe Leu Cys Leu Val Lys Tyr Gly Asn Leu Leu						
	210			215		220
Val Ser Gln Ile Phe Asn Trp Gln Lys Ser Glu Pro Gln Pro Ser Asn						
	225			230		235
Asn Gln Leu Trp Ile Ile Ile Leu Ser Ser Val Val Ser Gly Ile Val						
		245		250		255
Val Ile Thr Ala Leu Thr Leu Arg Cys Leu Val His Arg Pro Ala Ala						
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His Leu Ser Thr						
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ccc aag ctc ttt ccg ctc ttg atg cta gct agt ctt ttt tac ttc tgt	96
Pro Lys Leu Phe Pro Leu Leu Met Leu Ala Ser Leu Phe Tyr Phe Cys	
20 25 30	

146

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35 40 45	
tcc tgt gat tac aac att tcc acc aaa gaa ctg acg gaa att cga atc	192
Ser Cys Asp Tyr Asn Ile Ser Thr Lys Glu Leu Thr Glu Ile Arg Ile	
50 55 60	
tat tgg caa aag gat gat gaa atg gtg ttg gct gtc atg tct ggc aaa	240
Tyr Trp Gln Lys Asp Asp Glu Met Val Leu Ala Val Met Ser Gly Lys	
65 70 75 80	
gta caa gtg tgg ccc aag tac aag aac cgc aca ttc act gac gtc acc	288
Val Gln Val Trp Pro Lys Tyr Lys Asn Arg Thr Phe Thr Asp Val Thr	
85 90 95	
gat aac cac tcc att gtg atc atg gct ctg cgc ctg tca gac aat ggc	336
Asp Asn His Ser Ile Val Ile Met Ala Leu Arg Leu Ser Asp Asn Gly	
100 105 110	
aaa tac act tgt atc att caa aag att caa aaa ggg tct tac aaa gtg	384
Lys Tyr Thr Cys Ile Ile Gln Lys Ile Gln Lys Gly Ser Tyr Lys Val	
115 120 125	
aaa cac ctg act tcg gtg atg tta ttg gtc aga gct gac ttc cct gtc	432
Lys His Leu Thr Ser Val Met Leu Leu Val Arg Ala Asp Phe Pro Val	
130 135 140	
cct agt ata act gat ctt gga aat cca tct cat aac atc aaa agg ata	480
Pro Ser Ile Thr Asp Leu Gly Asn Pro Ser His Asn Ile Lys Arg Ile	
145 150 155 160	
atg tgc tta act tct gga ggt ttt cca aag cct cac ctc tcc tgg ctg	528
Met Cys Leu Thr Ser Gly Gly Phe Pro Lys Pro His Leu Ser Trp Leu	
165 170 175	
gaa aat gaa gaa gaa tta aat gcc atc aac aca aca gtt tcc caa gat	576
Glu Asn Glu Glu Glu Leu Asn Ala Ile Asn Thr Thr Val Ser Gln Asp	
180 185 190	
cct gaa act gag ctc tac act att agc agt gaa ctg gat ttc aat atg	624
Pro Glu Thr Glu Leu Tyr Thr Ile Ser Ser Glu Leu Asp Phe Asn Met	
195 200 205	
aca aac aac cat agc ttc ctg tgt ctt gtc aag tat gga aac tta ata	672
Thr Asn Asn His Ser Phe Leu Cys Leu Val Lys Tyr Gly Asn Leu Ile	
210 215 220	

gta tca cag atc ttc aac tgg caa aaa tca gag cca cag cct tct aat 720
 Val Ser Gln Ile Phe Asn Trp Gln Lys Ser Glu Pro Gln Pro Ser Asn
 225 230 235 240

aat cag ctc tgg atc att atc ctg agc tca gta gta agt ggg att gtt 768
 Asn Gln Leu Trp Ile Ile Ile Leu Ser Ser Val Val Ser Gly Ile Val
 245 250 255

gtg atc act gca ctt acc tta aga tgc cta gtc cac aga cct gct gca 816
 Val Ile Thr Ala Leu Thr Leu Arg Cys Leu Val His Arg Pro Ala Ala
 260 265 270

agg tgg aga caa aga gaa atg ggg aga gcg cgg aaa tgg aaa aga tct 864
 Arg Trp Arg Gln Arg Glu Met Gly Arg Ala Arg Lys Trp Lys Arg Ser
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cac ctg tct aca tag 879
 His Leu Ser Thr
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 35 40 45

Ser Cys Asp Tyr Asn Ile Ser Thr Lys Glu Leu Thr Glu Ile Arg Ile
 50 55 60

Tyr Trp Gln Lys Asp Asp Glu Met Val Leu Ala Val Met Ser Gly Lys
 65 70 75 80

Val Gln Val Trp Pro Lys Tyr Lys Asn Arg Thr Phe Thr Asp Val Thr
 85 90 95

Asp Asn His Ser Ile Val Ile Met Ala Leu Arg Leu Ser Asp Asn Gly
 100 105 110

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Met Gly Ile Cys Asp Ser Thr Met Gly Leu Ser His Thr Leu Leu	
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gtg atg gcc ctc ctg ctc tct ggt gtt tct tcc atg aag agt caa gca	155
Val Met Ala Leu Leu Leu Ser Gly Val Ser Ser Met Lys Ser Gln Ala	
20 25 30	
tat ttc aac aag act gga gaa ctg cca tgc cat ttt aca aac tct caa	203
Tyr Phe Asn Lys Thr Gly Glu Leu Pro Cys His Phe Thr Asn Ser Gln	
35 40 45	
aac ata agc ctg gat gag ctg gta gta ttt tgg cag gac cag gat aag	251
Asn Ile Ser Leu Asp Glu Leu Val Val Phe Trp Gln Asp Gln Asp Lys	
50 55 60	
ctg gtt ctg tat gag ata ttc aga ggc aaa gag aac cct caa aat gtt	299
Leu Val Leu Tyr Glu Ile Phe Arg Gly Lys Glu Asn Pro Gln Asn Val	
65 70 75	
cat ctc aaa tat aag ggc cgt aca agc ttt gac aag gac aac tgg acc	347
His Leu Lys Tyr Lys Gly Arg Thr Ser Phe Asp Lys Asp Asn Trp Thr	
80 85 90 95	
ctg aga ctc cac aat gtt cag atc aag gac aag ggc aca tat cac tgt	395
Leu Arg Leu His Asn Val Gln Ile Lys Asp Lys Gly Thr Tyr His Cys	
100 105 110	
ttc att cat tat aaa ggg ccc aaa gga cta gtt ccc atg cac caa atg	443
Phe Ile His Tyr Lys Gly Pro Lys Gly Leu Val Pro Met His Gln Met	
115 120 125	
agt tct gac cta tca gtg ctt gct aac ttc agt caa cct gaa ata aca	491
Ser Ser Asp Leu Ser Val Leu Ala Asn Phe Ser Gln Pro Glu Ile Thr	
130 135 140	
gta act tct aat aga aca gaa aat tct ggc atc ata aat ttg acc tgc	539
Val Thr Ser Asn Arg Thr Glu Asn Ser Gly Ile Ile Asn Leu Thr Cys	
145 150 155	
tca tct ata caa ggt tac cca gaa cct aag gag atg tat ttt cag cta	587
Ser Ser Ile Gln Gly Tyr Pro Glu Pro Lys Glu Met Tyr Phe Gln Leu	
160 165 170 175	
aac act gag aat tca act act aag tat gat act gtc atg aag aaa tct	635
Asn Thr Glu Asn Ser Thr Thr Lys Tyr Asp Thr Val Met Lys Lys Ser	
180 185 190	

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Phe	Asn	Lys	Thr	Gly	Glu	Leu	Pro	Cys	His	Phe	Thr	Asn	Ser	Gln	Asn	
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Ile	Ser	Leu	Asp	Glu	Leu	Val	Val	Phe	Trp	Gln	Asp	Gln	Asp	Lys	Leu	
	50					55					60					
Val	Leu	Tyr	Glu	Ile	Phe	Arg	Gly	Lys	Glu	Asn	Pro	Gln	Asn	Val	His	
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Leu	Lys	Tyr	Lys	Gly	Arg	Thr	Ser	Phe	Asp	Lys	Asp	Asn	Trp	Thr	Leu	
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Arg	Leu	His	Asn	Val	Gln	Ile	Lys	Asp	Lys	Gly	Thr	Tyr	His	Cys	Phe	
			100					105					110			
Ile	His	Tyr	Lys	Gly	Pro	Lys	Gly	Leu	Val	Pro	Met	His	Gln	Met	Ser	
		115					120					125				
Ser	Asp	Leu	Ser	Val	Leu	Ala	Asn	Phe	Ser	Gln	Pro	Glu	Ile	Thr	Val	
	130					135					140					
Thr	Ser	Asn	Arg	Thr	Glu	Asn	Ser	Gly	Ile	Ile	Asn	Leu	Thr	Cys	Ser	
	145				150					155					160	
Ser	Ile	Gln	Gly	Tyr	Pro	Glu	Pro	Lys	Glu	Met	Tyr	Phe	Gln	Leu	Asn	
			165						170					175		
Thr	Glu	Asn	Ser	Thr	Thr	Lys	Tyr	Asp	Thr	Val	Met	Lys	Lys	Ser	Gln	
		180						185					190			
Asn	Asn	Val	Thr	Glu	Leu	Tyr	Asn	Val	Ser	Ile	Ser	Leu	Pro	Phe	Ser	
		195					200					205				
Val	Pro	Glu	Ala	His	Asn	Val	Ser	Val	Phe	Cys	Ala	Leu	Lys	Leu	Glu	
	210					215					220					
Thr	Leu	Glu	Met	Leu	Leu	Ser	Leu	Pro	Phe	Asn	Ile	Asp	Ala	Gln	Pro	
	225				230					235					240	
Lys	Asp	Lys	Asp	Pro	Glu	Gln	Gly	His	Phe	Leu	Trp	Ile	Ala	Ala	Val	
				245					250					255		
Leu	Val	Met	Phe	Val	Val	Phe	Cys	Gly	Met	Val	Ser	Phe	Lys	Thr	Leu	
		260						265					270			

Arg Lys Arg Lys Lys Lys Gln Pro Gly Pro Ser His Glu Cys Glu Thr
275 280 285

Ile Lys Arg Glu Arg Lys Glu Ser Lys Gln Thr Asn Glu Arg Val Pro
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Tyr His Val Pro Glu Arg Ser Asp Glu Ala Gln Cys Val Asn Ile Leu
305 310 315 320

Lys Thr Ala Ser Gly Asp Lys Asn Gln
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<212> DNA

<213> feline CD28

<220>

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gta aca gaa aac aag att ttg gtg aag cag ttg ccc agg ctt gtg gtg 96
Val Thr Glu Asn Lys Ile Leu Val Lys Gln Leu Pro Arg Leu Val Val
20 25 30

tac aac aat gag gtc aac ctt agc tgc aag tac act cac aac ttc ttc 144
Tyr Asn Asn Glu Val Asn Leu Ser Cys Lys Tyr Thr His Asn Phe Phe
35 40 45

tca aag gag ttc cgg gca tcc ctt tat aag gga gta gat agt gct gtg 192
Ser Lys Glu Phe Arg Ala Ser Leu Tyr Lys Gly Val Asp Ser Ala Val
50 55 60

gaa gtc tgc gtt gtg aat gga aat tac tcc cat cag cct cag ttc tac 240
Glu Val Cys Val Val Asn Gly Asn Tyr Ser His Gln Pro Gln Phe Tyr
65 70 75 80

tca agt aca gga ttc gac tgt gat ggg aaa ttg ggc aat gaa aca gtg 288
Ser Ser Thr Gly Phe Asp Cys Asp Gly Lys Leu Gly Asn Glu Thr Val
85 90 95

11
153

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aca ttc tac ctc cga aat ttg ttt gtt aac caa acg gat att tac ttc 336
 Thr Phe Tyr Leu Arg Asn Leu Phe Val Asn Gln Thr Asp Ile Tyr Phe
 100 105 110

tgc aaa att gaa gtc atg tat cca cct cct tac ata gac aat gag aag 384
 Cys Lys Ile Glu Val Met Tyr Pro Pro Pro Tyr Ile Asp Asn Glu Lys
 115 120 125

agc aat ggg acc att atc cac gtg aaa gag aaa cat ctt tgt cca gct 432
 Ser Asn Gly Thr Ile Ile His Val Lys Glu Lys His Leu Cys Pro Ala
 130 135 140

cag ctg tct cct gaa tct tcc aag cca ttt tgg gca ctg gtg gtg gtt 480
 Gln Leu Ser Pro Glu Ser Ser Lys Pro Phe Trp Ala Leu Val Val Val
 145 150 155 160

ggc gga atc cta ggt ttc tac agc ttg cta gca aca gtg gct ctt ggt 528
 Gly Gly Ile Leu Gly Phe Tyr Ser Leu Leu Ala Thr Val Ala Leu Gly
 165 170 175

gct tgc tgg atg aag acc aag agg agt agg atc ctt cag agt gac tat 576
 Ala Cys Trp Met Lys Thr Lys Arg Ser Arg Ile Leu Gln Ser Asp Tyr
 180 185 190

atg aac atg acc ccc cgg agg cca ggg ccc acc cga agg cac tac caa 624
 Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Arg His Tyr Gln
 195 200 205

cct tac gcc cca gca cgc gac ttt gcg gca tac cgt tcc tgacatggac 673
 Pro Tyr Ala Pro Ala Arg Asp Phe Ala Ala Tyr Arg Ser
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Tyr Asn Asn Glu Val Asn Leu Ser Cys Lys Tyr Thr His Asn Phe Phe

12
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35 40 45
Ser Lys Glu Phe Arg Ala Ser Leu Tyr Lys Gly Val Asp Ser Ala Val
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Glu Val Cys Val Val Asn Gly Asn Tyr Ser His Gln Pro Gln Phe Tyr
65 70 75 80
Ser Ser Thr Gly Phe Asp Cys Asp Gly Lys Leu Gly Asn Glu Thr Val
85 90 95
Thr Phe Tyr Leu Arg Asn Leu Phe Val Asn Gln Thr Asp Ile Tyr Phe
100 105 110
Cys Lys Ile Glu Val Met Tyr Pro Pro Pro Tyr Ile Asp Asn Glu Lys
115 120 125
Ser Asn Gly Thr Ile Ile His Val Lys Glu Lys His Leu Cys Pro Ala
130 135 140
Gln Leu Ser Pro Glu Ser Ser Lys Pro Phe Trp Ala Leu Val Val Val
145 150 155 160
Gly Gly Ile Leu Gly Phe Tyr Ser Leu Leu Ala Thr Val Ala Leu Gly
165 170 175
Ala Cys Trp Met Lys Thr Lys Arg Ser Arg Ile Leu Gln Ser Asp Tyr
180 185 190
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195 200 205
Pro Tyr Ala Pro Ala Arg Asp Phe Ala Ala Tyr Arg Ser
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<212> DNA
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<220>
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<222> (27)..(698)

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12
155

5

~~14~~
156

SECRET

09303510.043099

190	195	200	
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Val Lys Met Pro Pro Thr Glu Pro Glu Cys Glu Lys Gln Phe Gln Pro			
205	210	215	
tat ttt att ccc atc aat tga cacaccgtta tgaagaagga agaacactgt			728
Tyr Phe Ile Pro Ile Asn			
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65	70	75	80
Met Thr Glu Val Cys Ala Ala Thr Tyr Thr Val Glu Asn Glu Leu Ala			
85	90	95	
Phe Leu Asn Asp Ser Thr Cys Thr Gly Ile Ser Ser Gly Asn Lys Val			
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Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile			
115	120	125	
Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Ala Gly Met Gly			
130	135	140	
Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser			
145	150	155	160

157

Asp Phe Leu Leu Trp Ile Leu Ala Ala Val Ser Ser Gly Leu Phe Phe
 165 170 175

Tyr Ser Phe Leu Ile Thr Ala Val Ser Leu Ser Lys Met Leu Lys Lys
 180 185 190

Arg Ser Pro Leu Thr Thr Gly Val Tyr Val Lys Met Pro Pro Thr Glu
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Pro Glu Cys Glu Lys Gln Phe Gln Pro Tyr Phe Ile Pro Ile Asn
 210 215 220

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0903510 07560660

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<400> 21
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<210> 57
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167

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atgggtcacg cagcaaagtg g

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<210> 73
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<400> 82
tcgaggatcc ttatttcgat gctctacggc etc 33

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